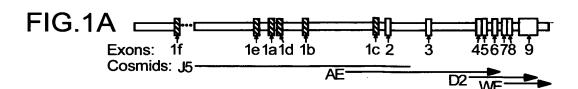
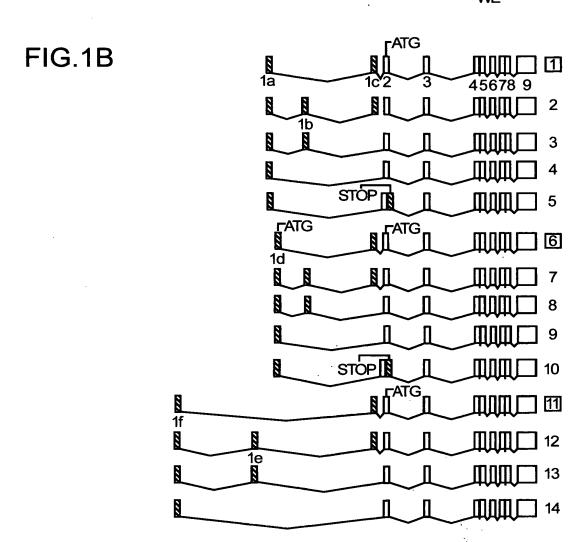


Title: Isoforms of the Human Vitamin D Receptor

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014





1 . . .



Title: Isoforms of the Human Vitamin D Receptor

(SEQ ID NO.15)-

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014

(SEQ ID NO.16) (SEQ ID NO.14)-

Transcript 1:
Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAWA ASTSL PDPGD FDRNV PRI DBD 427aa ▲
Transcript 9:
MEW RNKKR SDWLS MVLRTAGVEG MEAWA ASTSL PDPGD FDRNV PRI DBD 450aa ▲



Title: Isoforms of the Human Vitamin D Recer Inventor: Linda Anne Crofts

Application No.: 09/509,482 Docket No.: RICE-014

#### FIG. 4

- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

JAN 2 8 2003

Title: Isoforms of the Human Vitamin D Receptor Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

### FIG. 5A

<b>5</b> /		FIG. SA	<b>\</b>	
Transcrip	t 6			
<del>-</del>	Range: 1	to 1463)		
-	_			
10	20	30	40	50
* *	* *	* *	* *	* *
GTTTCCTTCT	TCTGTCGGGG	CGCCTTGGCA	TGGAGTGGAG	GAATAAGAAA
CAAAGGAAGA	AGACAGCCCC	GCGGAACCGT	ACCTCACCTC	CTTATTCTTT
				AsnLysLys>
		_		,
60	70	80	90	100
4 4	. , ,	4 4	4 4	100
		GGTGCTCAGA		
		CCACGAGTCT		
ArgSerAsp 1	TrpLeuSerMet	: ValLeuArg	ThrAlaGly \	/alGluGluAla>
110	120	130	140	150
* *		* *	* *	* *
Character	GAAGTGTCTG	TGAGACCTCA	CAGAAGAGCA	CCCCTGGGCT
•		ACTCTGGAGT		
		/alArgProHis		
Fliedlysel	GIUAGISEI /	dialgrionie	. wrawrawre	Fronendry
	486	100	400	000
160	170	180	190	200
* *	* *	* *	* *	* *
		CCTTCAGGGA		
GGTGAATGGA	CGGGGGACGA	GGAAGTCCCT	ACCTCCGTTA	CCGCCGGTCG
SerThrTyrLet	ı ProProAla	ProSerGly N	detGluAlaMe	t AlaAlaSer>
210	220	230	240	250
* *	* *	* *	* *	* *
y Caladio Conto	CHAST CCCARGG	AGACTTTGAC	CCCAACOTCC	CCCCCATCTC
		TCTGAAACTG		
inrserted 1	Proasprogr	A wabluewab	Argashval	ProArgIleCys>
260	270	280	290	300
* *	• •	* *	* *	* *
TGGGGTGTGT	<b>GGAGACCGAG</b>	CCACTGGCTT	TCACTTCAAT	GCTATGACCT
ACCCCACACA	CCTCTGGCTC	<b>GGTGACCGAA</b>	<b>AGTGAAGTTA</b>	CGATACTGGA
GlvValCvs	GlvAspArg	AlaThrGlyPho	e HisPheAsn	AlaMetThr>
310	320	330	340	350
310	320		340	
		TTCAGGCGAA		
		AAGTCCGCTT		
CysGluGlyCy	s LysGlyPhe	PheArgArg	SerMetLysAr	g LysklaLeu>
. 360	370	380	390	400
· • •		* *	* *	* *
TTCACCTGCC	CCTTCAACGG	GGACTGCCGC	ATCACCAAGG	ACAACCGACG
		GGACTGCCGC		
AAGTGGACGG	GGAAGTTGCC	CCTGACGGCG	TAGTGGTTCC	



### FIG. 5B

	440		420		430		440		450
	410		420		430	_	440		450
*	<b>*</b>	<b>-</b>				*			
		GCCTGCC							
		CGGACGG							
HisCy	sGln	AlaCysA	rg L	euLysA:	rgCys	: ValAs	pIle	GlyMet	Met>
	460		470		480		490		500
*	*	*	*	*	*	. *	*	*	*
AGGAGT	TCAT	TCTGACA	GAT	GAGGAA	GTGC	AGAGGA	AGCG	GGAGAT	GATC
TCCTCA	AGTA	AGACTGT	CTA	CTCCTT	CACG	TCTCCT	TCGC	CCTCTA	CTAG
LysGluP	helle	LeuThr	Asp	GluGlu'	Val (	SlnArgL	ysArg	g GluMe	tIle>
_			_						
	510		520		530		540		550
*	*	*	*	*	*	*	*	*	*
СТСААС	CCGA	AGGAGGA	GGA	GGCCTT	GAAG	GACAGT	СТСС	GGCCCA	AGCT
		TCCTCCT							
		LysGluGl							
neanys	mry i	Jy BGI UGI	uGIC	. Atabe	uLys	vapaer	weu a	AIGFIOD	y 3 Deu >
	560		<b>570</b>		E00		E00		600
	560	•	570 *	*	580		590		900
							-		
		CAGCAGC							
		GTCGTCG							
SerGl	uGlu	GlnGlnA	rg I	lelleA	laIle	e LeuLe	uAsp	AlaHis	His>
	610		620		630		640		650
*	*	*	*	*	*	*	*	*	*
		CCCCACC							
		GGGGTGG							
LysThrI	yrAsı	ProThr	Tyr	SerAsp	Phe (	CysGlnP	heAr	g ProPr	oVal>
	660		670		680		690		700
*	*	*	*	*	*	*	*	*	*
CGTGTG	AATG	ATGGTGG	AGG	GAGCCA	TCCT	TCCAGG	CCCA	ACTCCA	GACA
		TACCACC							
		AspGlyGl							
	710		720		730		740		750
	710	•	120		*	*	*	*	*
		TTCTCTC							
		AAGAGAC							
ThrPi	coSer	PheSerG	Sly A	AspSerS	erSe	r SerCy	sSer	Asphis	Cys>
	760		770		780		790		800
*	*	*	*	*	*	*	*	*	*
		AGACATO							
		TCTGTAC							
IleThr	SerSe	r AspMet	Met	AspSer	Ser	SerPheS	erAs	n LeuAs	pLeu>
	810		820		830		840		850
*	*	*	*	*	*	*	*	*	*
AGTGA	AGAAG	ATTCAGA	ATGA	CCCTTC	TGTG	ACCCTA	GAGC	TGTCCC	AGCT
		TAAGTC							
		AspSerAs							



## FIG. 5C

060	970	000	890	000
860	870	880	030	900
* *	* *	* *	* *	* *
CTCCATGCTG	CCCCACCTGG	CTGACCTGGT	CAGTTACAGC	ATCCAAAAGG
GAGGTACGAC	GGGGTGGACC	GACTGGACCA	GTCAATGTCG	TAGGTTTTCC
	ProHisLeu A			
Servernen	Frontspen 7	stavabnen.g.	Serryther	Tregrimys>
910	920	930	940	950
* *	* *	* *	* *	* *
ጥሮልጥጥረርርጥጥ	TGCTAAGATG	ATACCAGGAT	тсасасасст	CACCTCTGAG
	ACGATTCTAC			
VallleGlyPho	e AlaLysMet	IleProGly B	PheArgAspLeu	ThrSerGlu>
960	970	980	990	1000
* *	* *	* *	* *	* *
	TACTGCTGAA			
CTGGTCTAGC	ATGACGACTT	CAGTTCACGG	TAACTCCAGT	AGTACAACGC
AspGlnIle '	ValLeuLeuLvs	s SerSerAla	IleGluVal I	[leMetLeuArg:
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
CTCCAATGAG	TCCTTCACCA	TGGACGACAT	GTCCTGGACC	TGTGGCAACC
	AGGAAGTGGT			
SerAsnGlu	SerPheThr 1	MetAspAspMet	SerTrpThr	CysGlyAsn>
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
	cm> cccccmc		G033300000	101010000
	GTACCGCGTC			
TTCTGATGTT	CATGGCGCAG	TCACTGCACT	GGTTTCGGCC	TGTGTCGGAC
GlnAspTyrLy	s TyrArgVal	SerAspVal 7	ThrLysAlaGly	/ HisSerLeu>
		-	•	
1110	1120	1130	1140	1150
1110		1130	1140	1130
* *	* *	* *	* *	* *
GAGCTGATTG	AGCCCCTCAT	CAAGTTCCAG	GTGGGACTGA	AGAAGCTGAA
CTCGACTAAC	TCGGGGAGTA	GTTCAAGGTC	CACCCTGACT	TCTTCGACTT
				LysLysLeuAsn:
Graneatte ,	GIGLI OPERITY	= LysFileGin	valgryneu i	'A 2 DA 2 DE CW2!!
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
COOCCAOCAC	GAGGAGCATG	meenceene am	CCCCAMONGC	አጥተርጥተጥተር
	CTCCTCGTAC			
LeuHisGlu	GluGluHis '	ValLeuLeuMe	: AlaIleCys	IleValSer>
			_	
1210	1220	1230	1240	1250
1210	1220 * *	* *		
* *				
CAGATCGTCC	TGGGGTGCAG	GACGCCGCGC	TGATTGAGGC	CATCCAGGAC
GTCTAGCAGG	ACCCCACGTC	CTGCGGCGCG	ACTAACTCCG	GTAGGTCCTG
				a IleGlnAsp>
eroughurder	O GIANGIGIU	vahuraura (	DENTTEGINYT!	r rregringb.
1260	1270	1280	1290	1300
* *		* *		
00000000				
	ACACACTGCA			
GCGGACAGGT	TGTGTGACGT	CTGCATGTAG	GCGACGGCGG	TGGGCGGGGG
ArgLeuSer	AsnThrLeuGl:	n ThrTvrTle	ArgCvsArg 1	HisProProPro



Title: Isoforms of the Human Vitamin D Recentor

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014

#### FIG. 5D

1310 1320 1330 1340 1350 GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu> 1370 1360 1380 1390 1400 GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln> 1450 1410 1420 1430 1440 CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn> 1460 TGAGATCTCC TGA (SEQ ID NO:2) ACTCTAGAGG ACT (SEQ ID NO:17)

GluIleSer \*\*\*>(SEQ ID NO:9)



### FIG. 6A

Transcr	ipi	t 9			<b>O</b> ,	•			
	_	range:	1	to 138	21				
(ocque.		runge.		00 100			4.0		<b>5</b> 0
	10		20		30	•	40	•	50
- COMMENCA COM	-	momomooo				moon one		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	~~ ~ ~
GTTTCCTT		-							
CAAAGGAA	LGA	AGACAGCC	CC	GCGGAAC					
					P.	ietGluT1	. byt ć	, Marring	anya>
	60		70		80		90		100
*	*	*	*	*	*	*	*	*	*
AGGAGCGA	TT	GGCTGTCC	TAE	GGTGCTC	:AGA	ACTGCTC	GAG	TGGAGG	GGAT
TCCTCGCT									
ArgSerAs									
_	_	_			_		_		
1	110	1	L20		130		140		150
, ★	*	*	*	*	*	*	*	*	*
GGAGGCAA									
		CGCCGGT							
GluAlal	iet	AlaAlaSe	er 1	ChrSerLe	uPro	AspPro	Gly	AspPhe	Asp>
_					400		100		200
	160	•	170		180		190	•	200
CCD D CCTC	- -	CCGGATC	υ-⊃•υ •	eccenca	בייתביים	CAGACC	באמר	<u>ሮ</u> ልርጥርር	<b>Իւևուհւն</b> 
		GGCCTAG							
ArgAsnVal									
711 g1.51.1 4.2		, g		01,141	., .	orlinepi	- 9		, , , , , ,
2	210		220		230		240		250
*	*	*	*	*	*	*	*	*	*
CACTTCA	ATG	CTATGAC	CTG	TGAAGG	CTGC	AAAGGC!	rtct	TCAGGC	GAAG
GTGAAGT	TAC	GATACTG	GAC	ACTTCC	GACG	TTTCCG	AAGA	AGTCCG	CTTÇ
HisPheAs	sn 1	AlaMetTh:	rCy:	s GluGly	уСуs	LysGly	Phe 1	PheArgA	rgSer>
2	260	;	270		280		290		300
*	*	*	*	*	*	*	*	*	*
		AAGGCAC							
		TTCCGTG							
MetLys	Arg	LysAlaL	eu 1	PheThrC	ysPro	o PheAsi	nGly	AspCys.	Arg>
	210		222		224		340		350
•	310	•	320		330		<b>34</b> Ų	*	±
መርክ ርር አ እ		CAACCGA	_	-			ርርርጥ	CAAACG	רעיכיעי 
		GTTGGCT							
IleThrLy									
TTETHT NA	y Fla	h usmra	. r.+ Y	"TRCAS	٠,٠،٠ ،	uuyan	- 9 ~ 0		3-1-
	360		370		380		390		400
*	*	*	*	*	*		*	*	*
GTGGACA	TCG	GCATGAT	GAA	GGAGTT	CATT	CTGACA	GATG	AGGAAG	TGCA
		CGTACTA							
ValAspI	le (	GlyMetMe	tLy	s GluPh	eIle	LeuThr	Asp	GluGluV	alGln>
_			_				-		





## FIG. 6B

410	420	430	440	450
* *	* *	* *		* *
		TGAAGCGGAA		
		ACTTCGCCTT		
ArgLysArg	Glumetile i	LeuLysArgLys	GIUGIUGIU	AlaLeuLys>
460	470	480	490	500
* *	* *	* *	* *	* *
ACAGTCTGCG	GCCCAAGCTG	TCTGAGGAGC	AGCAGCGCAT	CATTGCCATA
TGTCAGACGC	CGGGTTCGAC	AGACTCCTCG	TCGTCGCGTA	GTAACGGTAT
AspSerLeuArg	ProLysLeu	SerGluGlu (	SlnGlnArgIle	e IleAlaIle>
510	520	530 * *	540	550
* *	* *			* *
		GACCTACGAC		
		CTGGATGCTG		
LeuLeuAsp A	итантентегу:	s Thriyrasp	Prountly	SerAspPheCys>
560	570	580	590	600
* *	* *			* *
CCAGTTCCGG	CCTCCAGTTC	GTGTGAATGA	TGGTGGAGGG	AGCCATCCTT
		CACACTTACT		
		ArgValAsnAsı		
_				
610	620			650
* *	* *	* *		* *
		ACTCCCAGCT		
		TGAGGGTCGA		
SerArgProAsi	n Serarghis	ThrProser	PneserGlyAs	p SerSerSer>
、 660	670	680	690	700
* *	* *	* *	* *	* *
ጥርርጥናርጥር AG	ATCACTGTAT			ACTCGTCCAG
		GTGGAGAAGT		
				AspSerSerSer>
<b>4</b>	- •			
710	720	730	740	750
* *	* *	* *	* *	* *
				CCTTCTGTGA
				GGAAGACACT
PheSerAsn	LeuAspLeu	SerGluGluAs	p SerAspAsp	ProSerVal>
	224	700	790	800
760	770	780	790	.* *
			CCCACCTGGC	TGACCTGGTC
				ACTGGACCAG
				a AspLeuVal>
···· TARAKATA				<b>&amp;</b>
810	820	830	840	850
* *	* *	* *	* *	* *
				TACCAGGATT
				ATGGTCCTAA
SerTyrSer	IleGlnLysVa	1 IleGlyPhe	AlaLysMet	IleProGlyPhe:



## FIG. 6C

860	870	880	890	900
* *	* *	088 * *	* *	* *
		ACCAGATCGT		
GTCTCTGGAG	TGGAGACTCC	TGGTCTAGCA	TGACGACTTC	AGTTCACGGT
		AspGlnIleVal		
gppc.c	importing .	.operrrc.u.		00100111101
910	920	930 * *	940	950
* *	* *	* *	* *	* *
mmca comea m		TCCAATGAGT		
		AGGTTACTCA		
IleGluValIle	e MetLeuArg	SerAsnGlu S	SerPheThrMet	: AspAspMet>
	_			
252	000	000	000	1000
960	970	980 * *	990	1000
* *	* *	* *	* *	* *
ጥሮርጥርርልርርጥ	GTGGCAACCA	AGACTACAAG	TACCGCGTCA	GTGACGTGAC
		TCTGATGTTC		
SerTrpThr (	CysGlyAsnGlı	n AspTyrLys	TyrArgVal S	SerAspValThr:
1010	1020	1020	1040	1050
1010	1020	1030	1040	1030
* *	* *	* *	* *	* *
CAAAGCCGGA	CACAGCCTGG	AGCTGATTGA	GCCCCTCATC	AAGTTCCAGG
		TCGACTAACT		
LysAlaGly	HisSerLeu (	GluLeuIleGlu	1 ProLeulle	LysPheGin>
1060	1070	1080	1090	1100
	* *	1080 * *	* *	* *
		TTGCATGAGG		
ACCCTGACTT	CTTCGACTTG	AACGTACTCC	TCCTCGTACA	GGACGAGTAC
				l LeuLeuMet>
vargry beaby.	o bybbcum.	Dedition (	3140141D	
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
		AGATCGTCCT		
		TCTAGCAGGA		
AlaIleCys	IleValSerPr	o AspArgPro	GlyValGln A	AspAlaAlaLeu:
			-	
11.00	1170	1180	1100	1200
1160	11/0	1100	1190	1200
* *	* *	* *	* *	* *
GATTGAGGCC	ATCCAGGACC	GCCTGTCCAA	CACACTGCAG	ACGTACATCC
				TGCATGTAGG
IleGluAla	IleGlnAsp .	ArgLeuSerAsı	n ThrLeuGln	ThrTyrIle>
1210	1220	1230	1240	1250
1210	1220		1240	
* *	* *	* *	* *	* *
GCTGCCGCCA	CCCGCCCCCG	GGCAGCCACC	TGCTCTATGC	CAAGATGATC
				GTTCTACTAG
ArgCysArgHi	s ProProPro	GlySerHis	LeuLeuTyrAl	a LysMetIle>
1260	1270	1280	1290	1300
	1210	1200	+ +	+ +
* *	* *	<b>4</b> 7	# #	
CAGAAGCTAG	CCGACCTGCG	CAGCCTCAAT	GAGGAGCACT	CCAAGCAGTA
GTCTTCGATC	GGCTGGACGC	GTCGGAGTTA	CTCCTCGTGA	GGTTCGTCAT
				SeriveCinfur



Title: Isoforms of the Human Vitamin D Recepta

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014

#### FIG. 6D

CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360 1370 1380

TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3) ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18) ValLeuGluVal PheGlyAsn GluIleSer \*\*\*> (SEQ ID NO:10)



## FIG. 7A

Transcrip	t 10				
(Sequence	Range: 1	to 1534)			
10	20	30	40	50	
* *	* *	* *	* *	* *	
	TCTGTCGGGG				
CAAAGGAAGA	AGACAGCCCC				
		M	letGluTrpArg	AsnLysLys>	
				100	
60	70	80	90	100	
,	GGCTGTCGAT	~ ~	» concomera e	mcca ccccam	
	CCGACAGCTA				
				alGluGlyMet>	
MIGDELMSP .	rtbreaservec	. varbeunry	111111111111111111111111111111111111111		
110	120	130	140	150	
* *	* *	* *	* *	* *	
GGAGGCAATG	GCGGCCAGCA	CTTCCCTGCC	TGACCCTGGA	GACTTTGACC	
CCTCCGTTAC	CGCCGGTCGT	GAAGGGACGG	ACTGGGACCT	CTGAAACTGG	
GluAlaMet	AlaAlaSer T	ChrSerLeuPro	AspProGly	AspPheAsp>	
160	170	180	190	200	
* *	* *	* *	* *	* *	
	CCGGATCTGT				
	GGCCTAGACA				
ArgAsnValPro	o ArglieCys	GlyvalCys (	SIYASPATGALA	ThrGlyPhe>	
210	220	230	240	250	
210	* *	* *	* *	* *	
CACTTC A ATC	CTATGACCTG	ጥርል ልርርርጥርር	AAAGGCTTCT	TCAGGTGAGC	
	GATACTGGAC				
				heArg*** (SEQ	ID NO:11)
				• • •	•
260	270	280	290	300	
* *	* . *	* *	* *	* *	
CCCCTCCCA	GGCTCTCCCC	AGTGGAAAGG	GAGGGAGAAG	AAGCAAGGTG	
GGGGGAGGGT	CCGAGAGGGG	TCACCTTTCC	CTCCCTCTTC	TTCGTTCCAC	
		•			
310	320	330	340	350	
* *	* *	* *	* *	* *	
	GGGAGCCCTT				
AAAGGTACTT	CCCTCGGGAA	CGTAAAAAGT	GTAGAGGAAG	GAATGTTACA	
360	270	380	390	400	
360	370	* *	* *	* *	
CCATGGAACA	TGCGGCGCTC	ACAGCCACAG	GAGCAGGAGG	GTCTTGGCGA	
				CAGAACCGCT	





# FIG. 7B

		1 10. 7 2		
410	420	430	440	450
AGCATGAAGC	GGAAGGCACT	A MINO A CICINO C	CCCMMCA A CC	COCACTOCOC
			CCCTTCAACG	
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC
4.00	4=4			
460	470	480	490	500
* *	* *	* *	* *	* *
CATCACCAAG	GACAACCGAC	GCCACTGCCA	GCCTGCCGG	CTCAAACGCT
GTAGTGGTTC	CTGTTGGCTG	CGGTGACGGT	CCGGACGGCC	GAGTTTGCGA
510	520	530	540	550
* *	* *	* *	* *	* *
GTGTGGACAT	CGGCATGATG	AAGGAGTTCA	TTCTGACAGA	TGAGGAAGTG
			AAGACTGTCT	
chenceloin	occorneine	11CC1CAAG1	MONCIOICI	ne recerrence
560	570	500	500	600
560	570	580	590	600
* *	* *	* *	* *	* *
CAGAGGAAGC	GGGAGATGAT	CCTGAAGCGG	AAGGAGGAGG	AGGCCTTGAA
GTCTCCTTCG	CCCTCTACTA	GGACTTCGCC	TTCCTCCTCC	TCCGGAACTT
610	620	630	640	650
* *	* *	* *	* *	* *
GGACAGTCTG	CGGCCCAAGC	TGTCTGAGGA	GCAGCAGCGC	ATCATTGCCA
			CGTCGTCGCG	
	0000001100		00.001000	
660	670	680	690	700
* *	* *		* *	* *
$m \ge \alpha m \alpha \alpha m \alpha \alpha s$	AAAAAA AAA M	1101000100	1000010001	
TACTGCTGGA		AAGACCTACG		
			ACCCCACCTA TGGGGTGGAT	
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG 750 * *
ATGACGACCT 710 * * TGCCAGTTCC	GCGGGTGGTA 720 * * GGCCTCCAGT	TTCTGGATGC 730 * * TCGTGTGAAT	TGGGGTGGAT 740 * *	GAGGCTGAAG 750 * * GGAGCCATCC
ATGACGACCT 710 * * TGCCAGTTCC	GCGGGTGGTA 720 * * GGCCTCCAGT	TTCTGGATGC 730 * * TCGTGTGAAT	TGGGGTGGAT  740  * * GATGGTGGAG	GAGGCTGAAG 750 * * GGAGCCATCC
ATGACGACCT 710 * * TGCCAGTTCC	GCGGGTGGTA 720 * * GGCCTCCAGT	TTCTGGATGC 730 * * TCGTGTGAAT	TGGGGTGGAT  740  * * GATGGTGGAG	GAGGCTGAAG 750 * * GGAGCCATCC
ATGACGACCT 710 * * * * * * * * * * * * * * * * * * *	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA	730  * TCGTGTGAAT AGCACACTTA	TGGGGTGGAT 740  * GATGGTGGAG CTACCACCTC	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG
ATGACGACCT 710 * TGCCAGTTCC ACGGTCAAGG 760 *	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * *	730  * * * * * * * * * * * * * * * * * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 *
TGCCAGTCC ACGGTCAAGG 760 * TTCCAGGCCC	720  * * GGCCTCCAGT CCGGAGGTCA  770  * AACTCCAGAC	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG	740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT
TGCCAGTCC ACGGTCAAGG 760 * TTCCAGGCCC	720  * * GGCCTCCAGT CCGGAGGTCA  770  * AACTCCAGAC	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT
ATGACGACCT 710 * TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG	730  * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC	TGGGGTGGAT  740  * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA
TGCCAGTCC ACGGTCAAGG 760 * TTCCAGGCCC	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG 820	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC	TGGGGTGGAT  740  * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA 850
ATGACGACCT 710 * TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 *	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * * AACTCCAGAC TTGAGGTCTG 820 * *	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC  830  *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * *
ATGACGACCT 710 * TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 *	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * * AACTCCAGAC TTGAGGTCTG 820 * *	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC  830  *	TGGGGTGGAT  740  * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * *
TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 * CCTCCTGCTC	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG 820 * AGATCACTGT	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC  830  * ATCACCTCTT	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * * GGACTCGTCC
TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 * CCTCCTGCTC	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG 820 * AGATCACTGT	730  * * TCGTGTGAAT AGCACACTTA  780  * ACACTCCCAG TGTGAGGGTC  830  * ATCACCTCTT	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * CAGACATGAT	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * * GGACTCGTCC
TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 * CCTCCTGCTC	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG 820 * AGATCACTGT	730  * * TCGTGTGAAT AGCACACTTA  780  * * ACACTCCAG TGTGAGGGTC  830  * ATCACCTCTT TAGTGGAGAA	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * * GGACTCGTCC CCTGAGCAGG
ATGACGACCT 710 * * TGCCAGTTCC ACGGTCAAGG 760 * TTCCAGGCCC AAGGTCCGGG 810 * CCTCCTGCTC GGAGGACGAG	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * * AACTCCAGAC TTGAGGTCTG 820 * * AGATCACTGT TCTAGTGACA	730  * * TCGTGTGAAT AGCACACTTA  780  * * ACACTCCAG TGTGAGGGTC  830  * ATCACCTCTT TAGTGGAGAA	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * * GACTCCTCCT CTGAGGAGGA 850 * * GGACTCGTCC CCTGAGCAGG
ATGACGACCT 710 * * * TGCCAGTTCC ACGGTCAAGG 760 * * * TTCCAGGCCC AAGGTCCGGG 810 * * CCTCCTGCTC GGAGGACGAG 860 *	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * * AACTCCAGAC TTGAGGTCTG 820 * * AGATCACTGT TCTAGTGACA 870 * *	730  * * TCGTGTGAAT AGCACACTTA  780  * * ACACTCCCAG TGTGAGGGTC  830  * * ATCACCTCTT TAGTGGAGAA  880  * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA 850 * GGACTCGTCC CCTGAGCAGG
ATGACGACCT 710 * * * * * * * * * * * * * * * * * * *	720  * * GGCCTCCAGT CCGGAGGTCA  770  * * AACTCCAGAC TTGAGGTCTG  820  * * AGATCACTGT TCTAGTGACA  870  * ATCTGGATCT	730  * * TCGTGTGAAT AGCACACTTA  780  * * ACACTCCCAG TGTGAGGGTC  830  * * ATCACCTCTT TAGTGGAGAA  880  * * GAGTGAAGAA	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * * GATTCAGATG	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA 850 * GGACTCGTCC CCTGAGCAGG 900 * ACCCTTCTGT
ATGACGACCT 710 * * * * * * * * * * * * * * * * * * *	720  * * GGCCTCCAGT CCGGAGGTCA  770  * * AACTCCAGAC TTGAGGTCTG  820  * * AGATCACTGT TCTAGTGACA  870  * ATCTGGATCT	730  * * TCGTGTGAAT AGCACACTTA  780  * * ACACTCCCAG TGTGAGGGTC  830  * * ATCACCTCTT TAGTGGAGAA  880  * * GAGTGAAGAA	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * *	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA 850 * GGACTCGTCC CCTGAGCAGG 900 * ACCCTTCTGT
TGCCAGTTCC ACGGTCAAGG  760  * TTCCAGGCCC AAGGTCCGGG  810  * CCTCCTGCTC GGAGGACGAG  860  * AGCTTCTCCA TCGAAGAGGT	720  * * GGCCTCCAGT CCGGAGGTCA  770  * AACTCCAGAC TTGAGGTCTG  820  * AGATCACTGT TCTAGTGACA  870  * ATCTGGATCT TAGACCTAGA	730  * * * * * * * * * * * * * * * * * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * GATTCAGATG CTAAGTTAC	GAGGCTGAAG 750 * * * * * * * * * * * * * * * * * * *
ATGACGACCT 710 * * * * * * * * * * * * * * * * * * *	720  * * GGCCTCCAGT CCGGAGGTCA  770  * AACTCCAGAC TTGAGGTCTG  820  * AGATCACTGT TCTAGTGACA  870  * ATCTGGATCT TAGACCTAGA	730  * * * * * * * * * * * * * * * * * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * * GATTCAGATG	GAGGCTGAAG 750 * * GGAGCCATCC CCTCGGTAGG 800 * GACTCCTCCT CTGAGGAGGA 850 * GGACTCGTCC CCTGAGCAGG 900 * ACCCTTCTGT
TGCCAGTTCC ACGGTCAAGG  760 * TTCCAGGCCC AAGGTCCGGG  810 * CCTCCTGCTC GGAGGACGAG  860 * AGCTTCTCCA TCGAAGAGGT	GCGGGTGGTA 720 * * GGCCTCCAGT CCGGAGGTCA 770 * AACTCCAGAC TTGAGGTCTG 820 * * AGATCACTGT TCTAGTGACA 870 * ATCTGGATCT TAGACCTAGA 920 *	730  * * * * * * * * * * * * * * * * * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * CAGACATGAT GTCTGTACTA  890  * GATTCAGATG CTAAGTCTAC  940  *	GAGGCTGAAG 750 * * * * * * * * * * * * * * * * * * *
TGCCAGTTCC ACGGTCAAGG  760 * TTCCAGGCCC AAGGTCCGGG  810 * CCTCCTGCTC GGAGGACGAG  860 * AGCTTCTCCA TCGAAGAGGT  910 GACCCTAGAG	GCGGGTGGTA  720  * * * * * * * * * * * * * * * * * *	TTCTGGATGC  730  * * * * * * * * * * * * * * * * * *	TGGGGTGGAT  740  * * GATGGTGGAG CTACCACCTC  790  * CTTCTCTGGG GAAGAGACCC  840  * * CAGACATGAT GTCTGTACTA  890  * GATTCAGATG CTAAGTTAC	GAGGCTGAAG  750  * * * * * * * * * * * * * * * * * *



# FIG. 7C

960	970	980	990 * *	1000
* *	* *	* *	* *	* *
TCAGTTACAG	CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA
			AACGATTCTA	
11010111010	01110011110			
1010	1020	1020	1040	1050
1010	1020	1030	1040	1030
TTCAGAGACC	TCACCTCTGA	GGACCAGATC	GTACTGCTGA	AGTCAAGTGC
AAGTCTCTGG	AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG
1000	1070	1000	1000	1100
1000	1070	1080	1090	1100
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	<b>ATGGACGACA</b>
GTAACTCCAG	TAGTACAACG	CGAGGTTACT	CAGGAAGTGG	TACCTGCTGT
		• • • • • •		
1110	1120	1120	1140	1150
1110	1120	1130	1140	1130
			AGTACCGCGT	
ACAGGACCTG	GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTCACTGCAC
***************************************				
1160	1170	1100	1100	1200
1160	11/0	1100	1190 * *	1200
* *	* *	* *	* *	
			GAGCCCCTCA	
TGGTTTCGGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210	1220	1230	1240	1250
1210	1220	1230	1240	+ +
ж т	* *			
			GGAGGAGCAT	
CCACCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
1200			1290 * *	* *
			CTGGGGTGCA	
ACCGGTAGAC	GTAGCAGAGG	GGTCTAGCAG	GACCCCACGT	CCTGCGGCGC
1310	1320	1330	1340	1350
		* *	* *	* *
			AACACACTGC	
GACTAACTCC	GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA
1360	1370	1380	1390	1400
* *		* *		
			CCTGCTCTAT	
GGCGACGGCG	GTGGGCGGG	GCCCGTCGGT	GGACGAGATA	CGGTTCTACT
	•			
1410	1420	1430	1440	1450
* +			* *	
	* *			
maa. a a.			AMCACCACCA	CONCLUS SACES OF
	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	
	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA TACTCCTCGT	
	AGCCGACCTG	CGCAGCCTCA	TACTCCTCGT	GAGGTTCGTC
	AGCCGACCTG TCGGCTGGAC	CGCAGCCTCA CGCTCGGAGT	TACTCCTCGT	GAGGTTCGTC
AGGTCTTCGA	AGCCGACCTG TCGGCTGGAC	CGCAGCCTCA CGCTCGGAGT	TACTCCTCGT	GAGGTTCGTC
AGGTCTTCGA	AGCCGACCTG TCGGCTGGAC	CGCAGCCTCA CGCGTCGGAGT	TACTCCTCGT	GAGGTTCGTC
AGGTCTTCGA 1460 * TACCGCTGCC	AGCCGACCTG TCGGCTGGAC 1470 * TCTCCTTCCA	CGCAGCCTCA CGCGTCGGAGT  1480  * GCCTGAGTGC	TACTCCTCGT  1490  * * * * * * * * * * * * * * * * * *	1500 * * *
AGGTCTTCGA 1460 * TACCGCTGCC	AGCCGACCTG TCGGCTGGAC 1470 * TCTCCTTCCA	CGCAGCCTCA CGCGTCGGAGT  1480  * GCCTGAGTGC	TACTCCTCGT	1500 * * *



#### FIG. 7D

1510 1520 1530

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4) ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)





10	20	30	40	50
≖ መድድሮ <b>እድድ</b> መውድ	*	# ####################################	~ CCMCA CCCCA	C) C) CCCCCCCCCCC
			GGTGAGGCCA CCACTCCGGT	
ACCCIOCAC	COCCACTCOO	ACCCCIGICC	CCACICCGGI	CICIGCCIGC
60	70	80	90	100
*	*	*	*	*
GACGCAGGGG	CCCGGCCCAA	GGCGAGGGAG	AACAGCGGCA	CTAAGGCAGA
CTGCGTCCCC	GGGCCGGGTT	CCGCTCCCTC	TTGTCGCCGT	GATTCCGTCT
110	120	130	140	150
*		*	*	*
			CCAATCCATC	
TTCCTTCTCC	CGCCACACAA	GTGGGCGTCG	GGTTAGGTAG	TGAGTCGTTG
160	170	100	100	200
160	170	180	190	200
TCCTAGACGC			GAGCCTGCCA	
			CTCGGACGGT	
710071701000	ROCALCITIC	HAGGAGGC1C	CICGGACGGI	AGGICAGCAC
210	220	230	240	250
*	*	*	+	*
CGTGCAGAAG	CCTTTGGGTC	TGAAGTGTCT	GTGAGACCTC	ACAGAAGAGC
GCACGTCTTC	GGAAACCCAG	ACTTCACAGA	CACTCTGGAG	TGTCTTCTCG
260	270	280	290	300
*	*	*	*	*
			TCCTTCAGGG	
TGGGGACCCG	AGGTGAATGG	ACGGGGGACG	AGGAAGTCCC	
				MetGluAla>
310	320	330	340	350
*	*	*	*	*
TGGCGGCCAG	CACTTCCCTG	CCTGACCCTG	GAGACTTTGA	CCGGAACGTG
			CTCTGAAACT	
				ArgAsnVal>
		•		
360	370	380	390	400
*	*	*	*	#
CCCCGGATCT			GCCACTGGCT	
			CGGTGACCGA	
ProArgIle	CysGlyValCy	s GlyAspArg	AlaThrGly	Ph <b>e</b> HisPheAsn>
410	400	4.00		450
410	420	430	440	450
* TCCMAMCA <i>C</i> C	#			*
			CTTCAGGCGA GAAGTCCGCT	
			GAAGTUCGUT e PheArgArg	
Tanecill	CAPOTAGTA	слапластльи	e rueargarg	2ettlechA2>
460	470	480	490	500
*	*	*	*	*
GGAAGGCACT	ATTCACCTGC	CCCTTCAACG	GGGACTGCCG	CATCACCAAG
			CCCTGACGGC	
				g IleThrLys>
<del></del>	•			-



#### FIG. 8B

510	520	530	540	550
GACAACCGAC	* GCCACTGCCA	GGCCTGCCGG	ም ርጥር እ እ አ ር ር ር ጥ	* CTCTCCACAT
		CCGGACGGCC		
				ysValAspIle>
	_			•
560	570	580	590	600
* ************************************	* እእሮሮእርመመርክ	# ####################################	# 	*
		TTCTGACAGA AAGACTGTCT		
		[leLeuThrAsp		
•	•			
610	620	630	640	650
*	*	*	*	*
		AAGGAGGAGG TTCCTCCTCC		
ArgGluMetIle				
ni goraneer r	Dearly	DySOLUGIU (	orania beary.	, inspectment
660	670	680	690	700
*	*	*	*	*
		GCAGCAGCGC		
		CGTCGTCGCG		
Argeronys i	senserGTMGT.	i Ginginarg	TIGITEMIA 1	[leLeuLeuAsp
710	720	730	740	750
*	*	*	•	*
		ACCCCACCTA		
		TGGGGTGGAT		
Alahishis	LysThrTyr A	AspProThrTy	r SerAspPhe	CysGlnPhe>
760	770	780	790	800
•	*	*	*	*
		GATGGTGGAG		
		CTACCACCTC		
Argeroprova.	L ArgvalAsn	Aspelyely (	GlySerHisPro	SerArgPro>
810	820	830	840	850
*	*	*	*	*
AACTCCAGAC	ACACTCCCAG	CTTCTCTGGG	GACTCCTCCT	CCTCCTGCTC
		GAAGAGACCC		
AsnSerArg I	HisThrProSe	r PheSerGly	AspSerSer S	SerSerCysSer:
860	870	880	890	900
*	*	*	*	900 *
AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC	AGCTTCTCCA
		GTCTGTACTA		
AspHisCys	IleThrSer	SerAspMetMet	t AspSerSer	SerPheSer>
_				
910	920	930	940	950 *
	CACTCAACAA	GATTCAGATG	_	
		CTAAGTCTAC		
				l ThrLeuGlu>
	r seratnata			
	u sergrugiu	nopocinop .	•	
960	u sergrugru 970		990	1000
960	970 *	980	990	1000
960 * CTGTCCCAGC	970 * TCTCCATGCT		990 * GCTGACCTGG	1000 * TCAGTTACAG



## FIG. 8C

1010	1020	1030	1040	1050
*	*	*	*	*
		TTGCTAAGAT		
		AACGATTCTA PheAlaLysMet		
Tredinnys	varifediy	enewrarysme (	. lierlogly	rneAtgAsp>
1060	1070	1080	1090	1100
*	*	*	*	*
		GTACTGCTGA CATGACGACT		
				GTAACTCCAG a IleGluVal>
nealimbergr	Applitte	varheuneu 1	naserserur	a TIEGIUVAI>
1110	1120	1130	1140	1150
*	*	*	*	*
		GTCCTTCACC		
		CAGGAAGTGG		
lleMetLeu /	ArgSerAsnGL	u SerPheThr	MetAspAsp I	MetSerTrpThr>
1160	1170	1180	1190	1200
*	*	*	*	*
		AGTACCGCGT		
		TCATGGCGCA		
CysGlyAsn	GlnAspTyr	LysTyrArgVal	l SerAspVal	ThrLysAla>
1210	1220	1230	1240	1250
*	*	*	±	*
		GAGCCCCTCA		
		CTCGGGGAGT		
GlyHisSerLe	ı GluLeuIle	GluProLeu 1	[leLysPheGl:	n ValGlyLeu>
1260	1270	1280	1290	1300
*	*	*	1250 *	*
AAGAAGCTGA	ACTTGCATGA	GGAGGAGCAT	GTCCTGCTCA	TGGCCATCTG
		CCTCCTCGTA		
LysLysLeu /	AsnLeuHisGl	u GluGluHis	ValLeuLeu 1	MetAlaIleCys>
1310	1320	1330	1340	1350
*	*	*	*	*
		CTGGGGTGCA		
		GACCCCACGT		
HeValSer	ProAspArg	ProGlyValGl	n AspAlaAla	LeulleGlu>
1360				
	1370	1380		1400
*	1370	1380	1390	1400
* CCATCCAGGA	CCGCCTGTCC	* AACACACTGC	1390 * AGACGTACAT	CCGCTGCCGC
CCATCCAGGA GGTAGGTCCT	CCGCCTGTCC GGCGGACAGG	* AACACACTGC TTGTGTGACG	1390  AGACGTACAT TCTGCATGTA	CCGCTGCCGC GGCGACGGCG
CCATCCAGGA GGTAGGTCCT	CCGCCTGTCC GGCGGACAGG	* AACACACTGC TTGTGTGACG	1390  AGACGTACAT TCTGCATGTA	CCGCTGCCGC
CCATCCAGGA GGTAGGTCCT AlalleGlnAs	CCGCCTGTCC GGCGGACAGG ArgLeuSer	AACACACTGC TTGTGTGACG AsnThrLeu	1390 *AGACGTACAT TCTGCATGTA GlnThrTyrIl	CCGCTGCCGC GGCGACGGCG e ArgCysArg>
CCATCCAGGA GGTAGGTCCT	CCGCCTGTCC GGCGGACAGG	* AACACACTGC TTGTGTGACG	1390  AGACGTACAT TCTGCATGTA	CCGCTGCCGC GGCGACGGCG
CCATCCAGGA GGTAGGTCCT AlalleGlnAsp	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420	AACACACTGC TTGTGTGACG AsnThrLeu (	1390  AGACGTACAT TCTGCATGTA GlnThrTyrll  1440  *	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450
CCATCCAGGA GGTAGGTCCT AlalleGlnAs; 1410 + CACCCGCCCC GTGGGCGGGG	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420 * CGGGCAGCCA GCCCGTCGGT	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA	1390  AGACGTACAT TCTGCATGTA GlnThrTyrlle  1440  GCCAAGATGA CGGTTCTACT	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450 TCCAGAAGCT AGGTCTTCGA
CCATCCAGGA GGTAGGTCCT AlalleGlnAs; 1410 + CACCCGCCCC GTGGGCGGGG	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420 * CGGGCAGCCA GCCCGTCGGT	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA	1390  AGACGTACAT TCTGCATGTA GlnThrTyrlle  1440  GCCAAGATGA CGGTTCTACT	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450 + TCCAGAAGCT
CCATCCAGGA GGTAGGTCCT AlalleGlnAs  1410  CACCCGCCCC GTGGGCGGGG HisProPro	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420 CGGGCAGCCA GCCCGTCGGT	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA s LeuLeuTyr	1390  AGACGTACAT TCTGCATGTA GINTHITYIII  1440  GCCAAGATGA CGGTTCTACT AlaLysMet	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450  TCCAGAAGCT AGGTCTTCGA IleGlnLysLeu>
CCATCCAGGA GGTAGGTCCT AlalleGlnAs; 1410 + CACCCGCCCC GTGGGCGGGG	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420 * CGGGCAGCCA GCCCGTCGGT	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA	1390  AGACGTACAT TCTGCATGTA GlnThrTyrlle  1440  GCCAAGATGA CGGTTCTACT	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450 TCCAGAAGCT AGGTCTTCGA IleGlnLysLeu>
CCATCCAGGA GGTAGGTCCT AlalleGlnAs  1410  CACCCGCCC GTGGGCGGG HisProPro  1460  *	CCGCCTGTCC GGCGGACAGG ArgLeuSer 1420 CGGGCAGCCA GCCCGTCGGT ProGlySerHi 1470	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA s LeuLeuTyr  1480 *	1390  AGACGTACAT TCTGCATGTA GINTHITYIII  1440  GCCAAGATGA CGGTTCTACT AlaLysMet  1490	CCGCTGCCGC GGCGACGGCG e ArgCysArg> 1450  TCCAGAAGCT AGGTCTTCGA IleGlnLysLeu> 1500 *
CCATCCAGGA GGTAGGTCCT AlalleGlnAs  1410  CACCCGCCC GTGGGCGGG HisProPro  1460  * AGCCGACCTG	CCGCCTGTCC GGCGGCACAGG ArgLeuSer 1420 CGGGCAGCCA GCCCGTCGGT ProGlySerHi 1470 * CGCAGCCTCA	AACACACTGC TTGTGTGACG AsnThrLeu  1430  * CCTGCTCTAT GGACGAGATA s LeuLeuTyr	1390  AGACGTACAT TCTGCATGTA GINTHITYIII  1440  GCCAAGATGA CGGTTCTACT AlaLysMet  1490  CTCCAAGCAG	CCGCTGCCGC GGCGACGGCG e ArgCysArg>  1450  TCCAGAAGCT AGGTCTTCGA IleGlnLysLeu>  1500  TACCGCTGCC
CCATCCAGGA GGTAGGTCCT AlalleGlnAs;  1410  CACCCGCCC GTGGGCGGGG HisProPro  1460  AGCCGACCTG TCGGCTGGAC	CCGCCTGTCC GGCGGCACAGG ArgLeuSer 1420 CGGGCAGCCA GCCCGTCGGT ProGlySerHi 1470 CGCAGCCTCA GCGTCGGAGT	AACACACTGC TTGTGTGACG AsnThrLeu  1430 * CCTGCTCTAT GGACGAGATA s LeuLeuTyr  1480 * ATGAGGAGCA	1390  AGACGTACAT TCTGCATGTA GINTHTTYRII  1440  GCCAAGATGA CGGTTCTACT AlaLysMet  1490  CTCCAAGCAG GAGGTTCGTC	CCGCTGCCGC GGCGACGGCG e ArgCysArg>  1450  TCCAGAAGCT AGGTCTTCGA IleGlnLysLeu>  TACCGCTGCC ATGGCGACGG



Title: Isoforms of the Human Vitamin D Receptor Inventor: Linda Anne Crofts

Application No.: 09/509,482 Docket No.: RICE-014

#### FIG. 8D

1510 1520 1530 1540 1550

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560 1570

GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7) CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20) ValPheGly AsnGlulleSer \*\*\*> (SEQ ID NO:12)

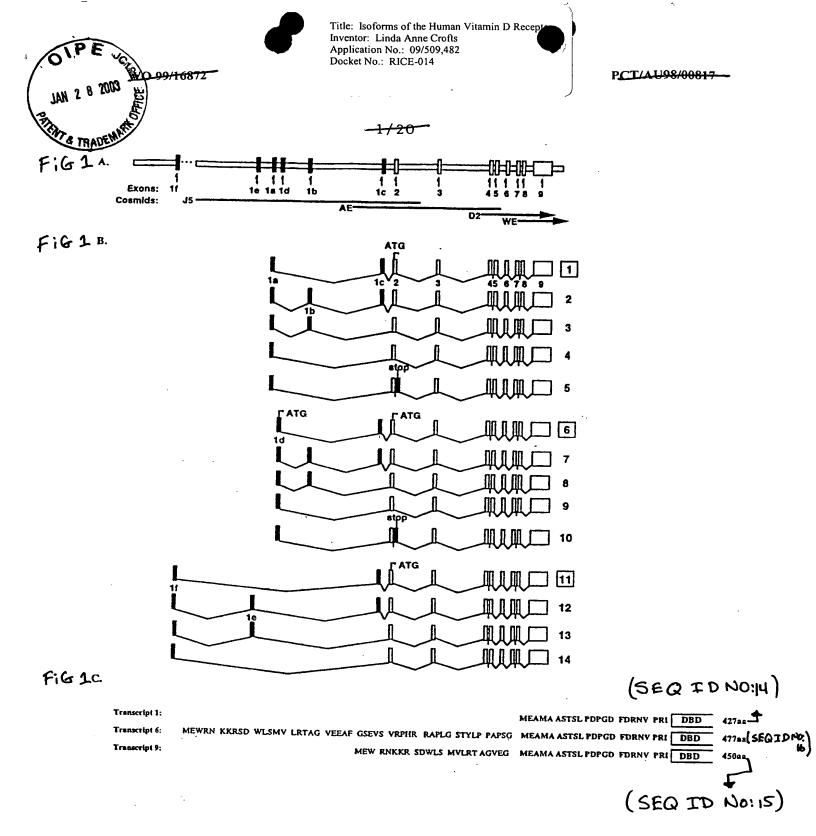


FIGURE 1

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014







- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC CGTGCACATTGCTTGCTTGCCTCCAATCCTCATAGCT TCTCTTTGGGgtaagtacag...3' (SEQ ID No:13
- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC CAGAGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG TTCACCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgttttttagAGGCAGCATGAAACAGTGGGATGTGCAGAG AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA CGGTATTTTTACTCTTCATGTCTGAAAAGGCTATGATAA AGATCAAgtaagatatt...3' (SEQ ID NO:6)
- 5'...GTTTCCTTCTGTCGGGGCGCCTTGGCATGGGAGTGG AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTGCTCA GAACTGCTGGAGTGGAGGgtgtgtaacc...3' ( SEQ ID HO! 1)



JAN 2 8 2003 FIG. 5A

5/20-

#### TRANSCRIPT 6

(Sequence Range: 1 to 1463)

10	20	30	40	50
* *	* *	* *	* *	* *
<b>G</b> かかかくないかくか	тстстссссс	CGCCTTGGCA	TGGAGTGGAG	GAATAAGAAA
		GCGGAACCGT		
CHINGGINGI	AGACAGCCCC			
		ž.	dereruit bar	g AsnLysLys>
,				4.5.5
60	70	80	90	100
* *	* *	* *	* *	* *
		GGTGCTCAGA		
		CCACGAGTCT		
ArgSerAsp 5	[rpLeuSerMet	t ValLeuArg	ThrAlaGly V	/alGluGluAla>
			•	
110	120	130	140	150
* *	. * *	* *	* *	* *
CTTTTCCCTCT	GAAGTGTCTG	TGAGACCTCA	CAGAAGAGCA	CCCCTGGGCT
		ACTCTGGAGT		
		ValArgProHi:		
PheGlysel	Gluvalsel	valArgeronis	s Algalgala	rroneagra>
1.00	170	180	190	200
160	170	180	190	200
* *	* *	* *		
		CCTTCAGGGA		
		GGAAGTCCCT		
SerThrTyrLe	u ProProAla	ProSerGly 1	MetGluAlaMe	t AlaAlaSer>
7	<b>V</b> '		· · · · · · · · · · · · · · · · · · ·	
210	220	230	240	250
* *	* *	* *	* *	* *
ACTTCCCTGC	CTGACCCTGG	AGACTTTGAC	CGGAACGTGC	CCCGGATCTG
TGAAGGGACG	GACTGGGACC	TCTGAAACTG	GCCTTGCACG	GGGCCTAGAC
				ProArgIleCys>
			_	
260	270	280	. 290	300
* *	* *	* *	* *	* *
THE CONTRACTOR	CCACACCCAC	CCACTGGCTT	ጥረ ልርጥጥረ ል ልጥ	CCTATCACCT
		GGTGACCGAA		
Gryvarcys	GIYASPATG	AlaThrGlyPh	e misrheash	Alametini
	200		240	250
310	320	330	340	350
* *	* *	* *	* *	* *
		TTCAGGCGAA		
				CTTCCGTGAT
CysGluGlyCy	s LysGlyPhe	PheArgArg	SerMetLysAr	g LysAlaLeu>
			•	
360	370	380	390	400
* *	* *	* * *	* *	* *
TTCACCTGCC	CCTTCAACGO	GGACTGCCGC	ATCACCAAGG	ACAACCGACG
AAGTGGACGG	GGAAGTTGCC	CCTGACGGCG	TAGTGGTTCC	TGTTGGCTGC
				AspAsnArgArg>
=			•	

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014

#### ₩<del>O 99/16872 </del>¬

PCT/AU98/00817



F16 5B 450 430 CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA GGTGACGGTC CGGACGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet> 490 500 460 470 480 AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle> 530 550 CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu> 570 580 590 600 GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis> 630 640 650 610 620 AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal> 700 690 680 660 670 CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis> 750 730 740 CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys> 790 760 770 780 TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu> 850 810 820 830 840 AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA

SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

Application No.: 09/509,482 Docket No.: RICE-014

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880 890 900 860 CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys> 930 940 950 910 920 TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu> 960 980 GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg> 1030 1040 1050 1010 1020 CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn> 1090 1070 1080 1100 1060 AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu> 1120 1130 1140 1150 1110 GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn> 1180 CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer> 1240 1210 1220 1230 \* CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp> 1300 CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>



Title: Isoforms of the Human Vitamin D Receptor,

Application No.: 09/509,482 Docket No.: RICE-014

#### WO-99/16872 -

Inventor: Linda Anne Crofts

PCT/AU98/00817-

#### FIG 5D

8/20

1330 GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

1380 1400 1360 1370

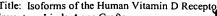
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

1450

CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

1460

TGAGATCTCC TGA (SEQ ID NO: 2) ACTCTAGAGG ACT (SEQ ED NO: 17) GluIleSer \*\*\*> (SEQ TO No. 9)



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TRANSCRIPT 9

(Sequence Range: 1 to 1382)

ange: I C	0 1.	304)							
								•	
_	10		20		30		40	*	50
*	*	*	*	. *					*
GTTTCCTT									
CAAAGGAA	GA A	AGACAGC	CCC	GCGGAA					
					M	MetGluT	rpArc	AsnLy	sLys>
	60		70		80		90		100
*	*	*	*	*	*	*	*	*	*
AGGAGCGA	TT	GGCTGTC	GAT	GGTGCT	CAGA	ACTGCT	GGAG	TGGAGG	GGAT
TCCTCGCT	'AA	CCGACAG	CTA	CCACGA	GTCT	TGACGA	CCTC	ACCTCC	CCTA
ArgSerAs									
	-	•			_		_		_
1	10		120		130		140		150
* -	*	*	*	*	*	*	*	*	*
GGAGGCAA	TYC:	CCCCCCA.	CCA	CTTCCC	ጥርርር	TGACCC	ТССА	GACTTT	GACC
CCTCCGTT									
GluAlaM									
Glualan	iet.	ATAATAS	er 1	miseir	euric	, waher	OGIA	vahtue.	usb>
			1 7 0		100		100		200
. 1	.60		170		180	4	190		200
*	*	*	*	*					
GGAACGTG									
CCTTGCAC									
ArgAsnVal	Pro	ArgIle	Cys	GlyVal	Cys (	GlyAspA	rgAla	a ThrGl	yPhe>
				•					
2	210		220		230		240		250
*	*	*	*	*	*	*	*	*	*
CACTTCAA	MTG	CTATGAC	CTG	TGAAGG	CTGC	AAAGGC	TTCT	TCAGGC	GAAG
GTGAAGTT	CAC	GATACTO	GAC	ACTTCC	GACG	TTTCCC	AAGA	AGTCCG	CTTC
HisPheAs	sn A	laMetTh	ırCys	s GluGl	уСуѕ	LysGly	Phe	PheArgA	rgSer>
			_						
2	260		270		280		290		300
*	*	*	*	*	*	*	*	*	*
CATGAAGO	CGG	AAGGCAC	TAT	TCACCT	GCCC	CTTCA	CGGG	GACTGC	CGCA
GTACTTC	300	TTCCGTG	מיתב	AGTGGA	CGGG	GAAGTT	rgccc	CTGACG	GCGT
Metive	A ~ ~	LysAlaI	مار	PhoThr(	ve Pr	o PheAs	nGlv	AspCvs	Ara>
меснуза	ar 9	Dyshiai	Jeu .	LICINIC	-y	0 111011			<b>J</b>
	310		320		330		340		350
	210		320	*	220	*	740	*	*
~~~~~	~~`	~ ~ ~ ~ ~ ~ ~ ~ ~				COMCC		CANACC	പ്രസ്വ
TCACCAA	GGA	CAACCGA	ACGC	CACTGO	CAGG	CCIGC	2000 1	CHARCO	CACA
AGTGGTT	CCT	GTTGGC.	IGCG	GIGACC	3GTCC	SCACO.	SCCGA Non-T-	GIIIG	-GACA
IleThrLy	sAsı	o AsnAr	gArg	Hiscys	eG'TU	AIACYS	argue	u LYSAI	.gcys>
									400
	360		370		380		390		400
*	*	*	*	*	*	*	*	*	*
GTGGACA'									
CACCTGT									
ValAspI	le (	GlyMetM	etLy	s GluPl	helle	LeuTh	rAsp	GluGluV	/alGln:





EVO 99/16872 JAN 2 8 2003

PC<del>T/AU98/00817 -</del>

	400	420	440	450
<b>410</b> * *	420 * *	430	· 440	450 * *
GAGGAAGCGG	GAGATGATCC	TGAAGCGGAA	GGAGGAGGAG	GCCTTGAAGG
CTCCTTCGCC	CTCTACTAGG	ACTTCGCCTT	CCTCCTCCTC	CGGAACTTCC
ArgLysArg	GluMetIle :	LeuLysArgLys	GluGluGlu	AlaLeuLys>
460	470	480	490	500
* *	* *	* *	* *	* *
ACAGTCTGCG	GCCCAAGCTG	TCTGAGGAGC	AGCAGCGCAT	CATTGCCATA
		AGACTCCTCG		
AspSerLeuArg	g ProLysLeu	SerGluGlu G	lnGlnArgIle	: IleAlaIle>
510	520	530	540	550
* *	* *	* *	* *	* *
CTGCTGGACG	CCCACCATAA	GACCTACGAC	CCCACCTACT	CCGACTTCTG
GACGACCTGC	GGGTGGTATT	CTGGATGCTG	GGGTGGATGA	GGCTGAAGAC
LeuLeuAsp 1	AlaHisHisLy	s ThrTyrAsp	ProThrTyr S	SerAspPheCys>
5.00	F70	E00	. 500	600
560 * *	570 * *	580 * *	* 590 * *	* *
CCAGTTCCGG	CCTCCAGTTC	GTGTGAATGA	TGGTGGAGGG	AGCCATCCTT
GGTCAAGGCC	GGAGGTCAAG	CACACTTACT	ACCACCTCCC	TCGGTAGGAA
GlnPheArg	ProProVal	ArgValAsnAsp	GlyGlyGly	SerHisPro>
	500	620	C40	650
610 * *	620 * *	630 * *	640 * *	650 * *
		ACTCCCAGCT	TCTCTGGGGA	CTCCTCCTCC
		TGAGGGTCGA		
SerArgProAs	n SerArgHis	ThrProSer H	heSerGlyAsp	SerSerSer>
	670	600	600	700
660 * *	670 * *		690 * *	700 * *
		CACCTCTTCA	GACATGATGG	ACTCGTCCAG
		GTGGAGAAGT		
SerCysSer	AspHisCysIl	e ThrSerSer	AspMetMet A	AspSerSerSer>
		<b>530</b>	7.40	750
710	720 * *		740 * *	750 * *
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		GTGAAGAAGA		
		CACTTCTTCT		
		SerGluGluAs		
			500	000
760 * *			790 * *	800 * *
		TCCATGCTGC		
		AGGTACGACG		
				a AspLeuVal>
•			2.12	252
810		830	840 * *	850 * *
AGTTACAGC	•	CATTGGCTTT		
TCAATGTCGT	AGGTTTTCC	A GTAACCGAAA	CGATTCTACT	ATGGTCCTAA
				IleProGlyPhe>

WO-99/16872

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FIG	,6C <sub>1-</sub>	<del>l/20</del>		
860	870	880	890	900
* *	* *	* *	* *	* *
CAGAGACCTC	ACCTCTGAGG	ACCAGATCGT	ACTGCTGAAG	TCAAGTGCCA
GTCTCTGGAG	TGGAGACTCC	TGGTCTAGCA	TGACGACTTC	AGTTCACGGT
ArgAspLeu	ThrSerGlu A	AspGlnIleVa	l LeuLeuLys	SerSerAla>
910	920	930	940	950
* *	* *	* *	* *	* *
<b>ጥጥር እ</b> ርረጥር እጥ	СУЛСТАСССС	ጥርር እ አጥር እርጥ	CCTTCACCAT	CCACCACAMO
				CCTGCTGTAC
IleGluValIle	e MetLeuArg	SerAsnGlu S	SerPheThrMe	t AspAspMet>
960	<b>97</b> 0	980	990	1000
* *	* *	* *	* *	* *
TCCTGGACCT	GTGGCAACCA	AGACTACAAG	TACCGCGTCA	GTGACGTGAC
AGGACCTGGA	CACCGTTGGT	TCTGATGTTC	ATGGCGCAGT	CACTGCACTG
SerTrpThr (	CysGlyAsnGl	n AspTyrLys	TyrArgVal S	SerAspValThr>
1010	1020	1020	1040	1050
* *	1020	1030	1040	1050
				* *
			GCCCCTCATC	
GTTTCGGCCT	GTGTCGGACC	TCGACTAACT	CGGGGAGTAG	TTCAAGGTCC
LysAlaGly	HisSerLeu (	GluLeuIleGlı	ı ProLeuIle	LysPheGln>
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
ጥርርር እርጥር እ እ	GAAGCTGAAC	ттссатсасс	AGGAGCATGT	<u> </u>
			TCCTCGTACA	
ValGlyLeuLys	s LysLeuAsn	Leunisgiu (	JIUGIUHISVA.	r LeuLeuMet>
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
GCCATCTGCA	TCGTCTCCCC	AGATCGTCCT	GGGGTGCAGG	ACGCCGCGCT
CGGTAGACGT	AGCAGAGGGG	TCTAGCAGGA	CCCCACGTCC	TGCGGCGCGA
				AspAlaAlaLeu>
1160	1170	1180	1190	1200
			CACACTGCAG	
			GTGTGACGTC	
IleGluAla	IleGlnAsp /	ArgLeuSerAsı	n ThrLeuGln	ThrTyrIle>
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
			TGCTCTATGC	
			ACGAGATACG	
ArgCysArgHi	s ProProPro	GlySerHis	LeuLeuTyrAla	a LysMetIle>
1260	1270	1280	1290	1300
* *	* *			* *
CAGAAGCTAAC	CCCACCTCCC		GAGGAGCACT	CCAACCACTA
			CTCCTCGTGA	GGTTCGTCAT

GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>

Title: Isoforms of the Human Vitamin D Receptor

Inventor: Linda Anne Crofts Application No.: 09/509,482 Docket No.: RICE-014

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FIG 6D 12/20

1310 1320 1330 1340 135

CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG GGCGACGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

1360 1370 1380

TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID No:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID No:18)
ValLeuGluVal PheGlyAsn GlulleSer \*\*\*> (SEQ ID No!10)

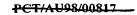




FIGURE 7

TRANSCRIPT 10

(Sequence Range: 1 to 1534)

ange. I co .				
10	20	30	40	50
* *	* *	* *	* *	* *
ርጥጥጥረረጥጥረጥ	<b>ТСТСТССССС</b>	CGCCTTGGCA	TGGAGTGGAG	GAATAAGAAA
		GCGGAACCGT		
C. L. L. C. C. L. C. L.				AsnLysLys>
		_		
60	70	80	90	100
* *	* *	* *	* *	* *
AGGAGCGATT	GGCTGTCGAT	GGTGCTCAGA	ACTGCTGGAG	TGGAGGGGAT
		CCACGAGTCT		
				/alGluGlyMet>
	_			
110	120	130	140	150
* *	* *	* *	* *	* *
GGAGGCAATG	GCGGCCAGCA	CTTCCCTGCC	TGACCCTGGA	GACTTTGACC
		GAAGGGACGG		
GluAlaMet	AlaAlaSer '	ThrSerLeuPro	o AspProGly	AspPheAsp>
160	170	180	190	200
* *	* *	* *	* *	* *
GGAACGTGCC	CCGGATCTGT	GGGGTGTGTG	GAGACCGAGC	CACTGGCTTT
CCTTGCACGG	GGCCTAGACA	CCCCACACAC	CTCTGGCTCG	GTGACCGAAA
ArgAsnValPr	o ArgIleCys	GlyValCys (	GlyAspArgAla	a ThrGlyPhe>
				0.50
210	220	230	240	250
* *	* *	* *	* *	* *
CACTTCAATG	CTATGACCTG	TGAAGGCTGC	AAAGGCTTCT	TCAGGTGAGC
GTGAAGTTAC	GATACTGGAC	ACTTCCGACG	TTTCCGAAGA	AGICCACICG
HisPheAsn	AlaMetThrCy	s GluGlyCys	LysGIyPne	Pneargana
250	050	280	290	300
260	270		± ±	* *
* *		AGTGGAAAGG	CACCCACAAC	A ACCA ACCTG
CCCCCTCCCA	GGCTCTCCCC	TCACCTTTCC	CTCCCTCTTC	THECHTECAC
GGGGGAGGGT	CCGAGAGGGG	TCACCITICC	CICCCICIIC	TICGLICCAC
310	320	330	340	350
* *	. * *	* * *	* *	* *
<b>ጥጥጥርር አጥር አ</b> አ	GGGAGCCCT1	GCATTTTTCA	CATCTCCTTC	CTTACAATGT
				GAATGTTACA
ILLUGIACI			<del></del>	
360	370	380	390	400
* 1	k # 1	e ste st	* *	* *
CCATGGAACA	TGCGGCGCTC	ACAGCCACAG	GAGCAGGAGG	GTCTTGGCGA
				CAGAACCGCT

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FIG 75	3 14	120		
410	420	430	•	450
		ATTCACCTGC	* * CCCTTCAACG	
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC
460 * *	470 * *	480 * *	490 * *	500 * *
			GGCCTGCCGG CCGGACGGCC	
510 * *	520 * *	530 * *	540 * *	550 * *
		AAGGAGTTCA	TTCTGACAGA AAGACTGTCT	TGAGGAAGTG
560	570			
* * CAGAGGAAGC	* * GGGAGATGAT	* * CCTGAAGCGG	* * AAGGAGGAGG	* * AGGCCTTGAA
			TTCCTCCTCC	-
610	620	630	640	650 * *
			* * GCAGCAGCGC	
			CGTCGTCGCG	
660 * *	670 * *	680 * *	690 * *	700 * *
TACTGCTGGA	CGCCCACCAT		ACCCCACCTA	
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
710	720	730	740	750 * *
* *	* *		* * GATGGTGGAG	
	CCGGAGGTCA		CTACCACCTC	
760	770 * *	780 * *	790 * *	800
TTCCAGGCCC			CTTCTCTGGG	GACTCCTCCT
			GAAGAGACCC	
810 * *	820 * *	* * *	840 * *	850 * *
CCTCCTGCTC	AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC
			GTCTGTACTA	
860	870 * *		890 * *	• 900 * *
AGCTTCTCCA			GATTCAGATG	
			CTAAGTCTAC	
910				
* * * CACCCTACAC	* * *		* * GCCCCACCTG	
			CGGGGTGGAC	



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FIG 7C

J C 1 -		<del>25/2</del> 0		•
960 * *	970 * *	980	990	1000
			TTGCTAAGAT	
			AACGATTCTA	
1010			1040	
			GTACTGCTGA	
AAGTCTCTGG	AGTGGAGACT		CATGACGACT	
1060	1070 * *	1080	1090 * *	1100 * *
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	ATGGACGACA
			CAGGAAGTGG	
1110	1120	1130	1140	1150
* *	+ +	* *	* *	1130
			AGTACCGCGT	
			TCATGGCGCA	
1160	1170	1180	1190 * *	1200
* *	* *	* *	* *	* *
ACCAAAGCCG	GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA
TGGTTTCGGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210		1230	1240 * *	
GGTGGGACTG	AAGAAGCTGA	ACTTGCATGA	GGAGGAGCAT	GTCCTGCTCA
CCACCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
			CTGGGGTGCA	
			GACCCCACGT	
1310	1320 * *	1330	1340	
CTGATTGAGG	GGTAGGTCCT	GGCGGACAGG	AACACACTGC TTGTGTGACG	TCTGCATGTA
1360			1390 * *	
			CCTGCTCTAT	
•			GGACGAGATA	
1410	1420	1430	1440	1450
* *	* *	* *	* *	* *
			ATGAGGAGCA TACTCCTCGT	
1460		1480		
* *	* *	* *	* *	* *
				TAACGCCCCT ATTGCGGGGA

Title: Isoforms of the Human Vitamin D Receptor

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FIG 7D

1510

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA ( SEQ ID 1014) ACACGAGCTT CACAAACCGT TACTCTAGAG GACT ( SEQ ID NO: 19)

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FIGBA

FIGURE 8	TRANSO	CRIPT 11		
10	20	30	40	50
* ፕሮርርልርርፕፕር	* GCGGTGAGCC	* TCCCCACACA	*	*
ACGCTGGAAC	CGCCACTCGG	ACCCCTGTCC	CCACTCCGGT	CTCTGCCTGC
60 *	70 *	80	90	100
GACGCAGGGG CTGCGTCCCC	CCCGGCCCAA GGGCCGGGTT	GGCGAGGGAG CCGCTCCCTC	AACAGCGGCA TTGTCGCCGT	CTAAGGCAGA GATTCCGTCT
110	120	130	140	150 *
AAGGAAGAGG TTCCTTCTCC	GCGGTGTGTT CGCCACACAA	CACCCGCAGC GTGGGCGTCG	CCAATCCATC GGTTAGGTAG	ACTCAGCAAC TGAGTCGTTG
160 *	170 *	180	190	200
TCCTAGACGC AGGATCTGCG	TGGTAGAAAG ACCATCTTTC	TTCCTCCGAG AAGGAGGCTC	GAGCCTGCCA CTCGGACGGT	TCCAGTCGTG AGGTCAGCAC
210	220	230	240	250 *
CGTGCAGAAG GCACGTCTTC	CCTTTGGGTC GGAAACCCAG	TGAAGTGTCT ACTTCACAGA	GTGAGACCTC CACTCTGGAG	ACAGAAGAGC TGTCTTCTCG
260	270 *	280	290	300 *
ACCCCTGGGC TGGGGACCCG	TCCACTTACC AGGTGAATGG	TGCCCCCTGC ACGGGGGACG	TCCTTCAGGG AGGAAGTCCC	ATGGAGGCAA TACCTCCGTT MetGluAla>
310 *	320 *	330	340	350 *
TGGCGGCCAG ACCGCCGGTC MetAlaAlaSe	CACTTCCCTG GTGAAGGGAC ThrSerLeu	GGACTGGGAC	CTCTGAAACT	GGCCTTGCAC
360	370	380	390	400
CCCCGGATCT	GTGGGGTGTG	TGGAGACCGA	GCCACTGGCT	* TTCACTTCAA
ProArgIle (	CACCCCACAC CysGlyValCys	ACCTCTGGCT s GlyAspArg	CGGTGACCGA AlaThrGly I	AAGTGAAGTT PheHisPheAsn>
410	420	430	440	450
ACGATACTGG	TGTGAAGGCT ACACTTCCGA CysGluGly	CGTTTCCGAA	GAAGTCCGCT	TCGTACTTCG
460 *	470 *	480	490	500 *
GGAAGGCACT CCTTCCGTGA ArgLysAlaLeu	ATTCACCTGC TAAGTGGACG PheThrCys	CCCTTCAACG GGGAAGTTGC	CCCTGACGGC	GTAGTGGTTC

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FIG 8B

520 540 550 530 GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle> 560 570 580 600 CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys> 610 620 630 GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu> 660 670 680 690 700 CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp> 710 720 730 740 750 CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe> 760 780 790 800 GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro> 810 820 830 840 850 AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer> 860 870 880 890 900 AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer> 910 920 930 940 950 ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu> 960 980 990 CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC

LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>

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FIG BC 1020 1030 1040 1050 CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp> TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal> 1120 1130 1150 ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr> 1160 1170 1180 1190 1200 CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla> 1210 1220 1230 1240 1250 GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu> 1260 1270 1280 1300 AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys> 1310 1320 1330 1340 1350 CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu> 1360 1370 1380 1390 1400 CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg> 1410 1420 1430 1440 1450 CACCCGCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT GTGGGCGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu> 1470 1480

AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

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Title: Isoforms of the Human Vitamin D Recepto

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FIGBD

20/20

1510

1520

1530

1540

1550

TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560

1570

CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: 7)
ValPheGly AsnGlulleSer \*\*\*> (SEQ ID NO: 12)